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SUMMARY OF THESIS

XAVIER, Paula Cristhina Niz - **Análise epidemiológica e molecular de candidemia em pacientes internados no NHU-UFMS, 1998-2006**. Campo Grande, 2008. (Dissertação de Mestrado - Universidade Federal de Mato Grosso do Sul).

EPIDEMIOLOGY AND MOLECULAR ANALYSIS OF CANDIDEMIA IN IN-PATIENTS OF THE NHU-UFMS, 1998-2006

The incidence of bloodstream (BSI) *Candida* infections has increased in the last years. Studies carried out in several countries have shown differences in the epidemiology of the invasive infections caused by this yeast. In the Center-West region of Brazil, data about candidemia are still scarce. This pathology is associated with high mortality (30% to 60%) and with longer hospital stay. We have carried out a retrospective analysis of cases of *Candida* BSI in a tertiary teaching hospital in Mato Grosso do Sul, Brazil, to study the clinical and epidemiological aspects of the disease and to determine the genetic similarity of the yeasts isolated through PCR-RAPD assay. Ninety-six cases of *Candida* spp. BSI, reported between January 1998 and December 2006, were included in the study. The patients' age ranged from three days to 85 years; 53 (55.2%) adults and 43 (44.8%) children. They have been in hospital for a period ranging from one to 124 days, with an average of 30 days. Candidemia episodes were recorded most at adult ICU (n = 29; 30.1%) and newborn ICU (n = 25; 26.0).Among the pediatrics, 23 were newborns. Seventeen neonates (68%) had birth weight lower than 1500 g. Fifty-eight patients (60.4%) died during hospital stay. The main associated conditions were: hospital stay longer than 15 days (n = 66; 68.8%), catheter in central position (61; 63.5%) and use of third-generation cephalosporins (n = 55; 57.3%). Among the pediatric patients, five (11.6%) presented with congenital malformation and twelve (27.9%) with perinatal infection. The most frequent1y reported base illnesses were: Diabetes Mellitus (10.4%), solid tumor (9.4%) and hematological diseases (12.5%). The most common agents were: *Candida albicans* (45.8%), *Candida parapsilosis* (34.4%), *Candida tropicalis* (14.6%) and *Candida glabrata* (5.2%). The amplification of genomic DNA of the isolated yeasts gave origin to a large variety of genetic profiles among the different species of *Candida* and among the strains of the same species, proving the high discriminatory power of the technique. This is the first description of bloodstream infection caused by *Candida* species in Mato Grosso do Sul, Brazil, and confirms the importance of the clinical suspicion of invasive *Candida* spp. infections in the patients' evolution, especially when elderly patients and neonates are involved.

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